

SEQUENCE LISTING

<110> WILEY, Steven R.

<120> TWEAK Receptor

<130> 2968-B

<140> to be assigned

<141> 2000-12-19

<150> 60/172,878

<151> 1999-12-20

<150> 60/203,347

<151> 2000-05-10

<160> 7

<170> PatentIn Ver. 2.0

<210> 1

<211> 898

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (52)..(873)

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<223> Description of Artificial Sequence: human TWEAK
fusion protein construct

<400> 1

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                                     Met Ala
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aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc ctg ctc tgc ctg 105
Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
      5                      10                      15

ccc tgg ctt caa gag ggc agt gca act agt tct gac cgt atg aaa cag 153
Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met Lys Gln
      20                      25                      30

ata gag gat aag atc gaa gag atc cta agt aag att tat cat ata gag 201
Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu
      35                      40                      45                      50

aat gaa atc gcc cgt atc aaa aag ctg att ggc gag cgg act aga tct 249
Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Arg Ser
      55                      60                      65

agt ttg ggg agc cgg gca tcg ctg tcc gcc cag gag cct gcc cag gag 297
Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu
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<211> 273
<212> PRT
<213> Artificial Sequence
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His

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<221> CDS
<222> (53) .. (442)
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Met Ala

cgg ggc tcg ctg cgc cgg ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg 106
 Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly Leu Trp
 5 10 15

ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc acc gcc 154
 Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly Thr Ala
 20 25 30

ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag tgc atg 202
 Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys Cys Met
 35 40 45 50

gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc ctg ggc 250
 Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys Leu Gly
 55 60 65

tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg ccc atc ctt 298
 Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu
 70 75 80

ggg ggc gct ctg agc ctg acc ttc gtg ctg ggg ctg ctt tct ggc ttt 346
 Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser Gly Phe
 85 90 95

ttg gtc tgg aga cga tgc cgc agg aga gag aag ttc acc acc ccc ata 394
 Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile
 100 105 110

gag gag acc ggc gga gag ggc tgc cca gct gtg gcg ctg atc cag tga 442
 Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile Gln
 115 120 125 130

caatgtgccc cctgccagcc ggggctcgcc cactcatcat tcattcatcc attctagagc 502

cagtctctgc ctcccagacg cggcggggagc caagctcttc caaccacaag ggggggtgggg 562

ggcggtgaat cacctctgag gcctggggccc aggggttcagg ggaaccttcc aagggtgtctg 622

gttgccctgc ctctggctcc agaacagaaa gggagcctca cgctgggtca cacaaaacag 682

ctgacactga ctaaggaact gcagcatttg cacaggggag ggggggtgccc tccttcctag 742

aggccctggg ggccaggctg acttggggggg cagacttgac actaggcccc actcactcag 802

atgtcctgaa attccaccac ggggggtcacc ctgggggggtt agggacctat ttttaacact 862

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<212> PRT

<213> Homo sapiens

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Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35 40 45
 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
 50 55 60
 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
 65 70 75 80
 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
 85 90 95
 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
 100 105 110
 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
 115 120 125

Gln

<210> 5
 <211> 129
 <212> PRT
 <213> Mus sp.

<400> 5
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 Phe Gly Leu Val Leu Met Arg Ala Ala Ala Gly Glu Gln Ala Pro Gly
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 Thr Ser Pro Cys Ser Ser Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35 40 45
 Cys Met Asp Cys Ala Ser Cys Pro Ala Arg Pro His Ser Asp Phe Cys
 50 55 60
 Leu Gly Cys Ala Ala Ala Pro Pro Ala His Phe Arg Leu Leu Trp Pro
 65 70 75 80
 Ile Leu Gly Gly Ala Leu Ser Leu Val Leu Val Leu Ala Leu Val Ser
 85 90 95
 Ser Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
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 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Gly Val Ala Leu Ile
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Gln

<210> 6
 <211> 932
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS

<222> (1)..(930)

<220>

<223> Description of Artificial Sequence: human TWEAK
receptor fusion protein construct

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ctc tgg ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc	96
Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly	
20 25 30	
acc gcc ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag	144
Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys	
35 40 45	
tgc atg gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc	192
Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys	
50 55 60	
ctg ggc tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg aga	240
Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Arg	
65 70 75 80	
tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc	288
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala	
85 90 95	
gag ggc gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc	336
Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr	
100 105 110	
ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg	384
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val	
115 120 125	
agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg	432
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val	
130 135 140	
gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc	480
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser	
145 150 155 160	
acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg	528
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu	
165 170 175	
aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc	576
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala	
180 185 190	
ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca	624
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro	
195 200 205	
cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag	672
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln	
210 215 220	

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gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc 720
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
225 230 235 240

gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg 768
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
245 250 255

cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat agc aag ctc 816
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
260 265 270

acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc 864
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
275 280 285

gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc 912
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
290 295 300

ctg tct ccg ggt aaa tga ac 932
Leu Ser Pro Gly Lys
305 310

<210> 7
<211> 309
<212> PRT
<213> Artificial Sequence

<400> 7
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Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
20 25 30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
35 40 45

Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
50 55 60

Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Arg
65 70 75 80

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
85 90 95

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
100 105 110

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
115 120 125

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
130 135 140

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
145 150 155 160

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006T2T "45424260

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
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 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 180 185 190
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 195 200 205
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 210 215 220
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 225 230 235 240
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 245 250 255
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 260 265 270
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 275 280 285
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 290 295 300
 Leu Ser Pro Gly Lys
 305

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